

Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 other;

Query Match	100.0%	Score 1008	DB 21	Length 1076
Best Local Similarity	100.0%	Pred. No. 1.6e-302		
Matches 1008	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	atggctgggtcccccacacatgctcacctcatctatctctttggcagctcacagggtca	60	
Db	38	atggctgggtcccccacacatgctcacctcatctatctctttggcagctcacagggtca	97	
QY	61	gagcctctggaccogtgaagagctgggtcogttcogttggtggggcogtgactttcccc	120	
Db	98	gagcctctggaccogtgaagagctgggtcogttcogttggtggggcogtgactttcccc	157	
QY	121	ctgaagtcacaaagtaaacgaagttgactctattgtctggaccttcacacacacccctctt	180	
Db	158	ctgaagtcacaaagtaaacgaagttgactctattgtctggaccttcacacacacccctctt	217	
QY	181	gtcacccatcacagcagaaggggcacctcatctatgtgacccaaaatcgttaataggagaga	240	
b	218	gtcacccatcacagcagaaggggcacctcatctatgtgacccaaaatcgttaataggagaga	277	
QY	241	gtagacttcccagatgagggtactcctgaagctcagcaactgaagaataactgactca	300	
Db	278	gtagacttcccagatgagggtactcctgaagctcagcaactgaagaataactgactca	337	
QY	301	gggactactatgtgggatatcacagctcatcactccagcagccctccacccaggagtac	360	
Db	338	gggactactatgtgggatatcacagctcatcactccagcagccctccacccaggagtac	397	
QY	361	gtgctgcatgtctacgacgacactgtcaaaagctcaaaagctcaccatgggtcgcagagcaat	420	
Db	398	gtgctgcatgtctacgacgacactgtcaaaagctcaaaagctcaccatgggtcgcagagcaat	457	
QY	421	aagaatgagcactgtgtgaccaaatctgaactgtcgtcgtcgaacatggggaagagatgtg	480	
Db	458	aagaatgagcactgtgtgaccaaatctgaactgtcgtcgtcgaacatggggaagagatgtg	517	
QY	481	attatatactggaaagccctggggcagcagcagcgaatgagtcacataatgggtccatctctc	540	
Db	518	attatatactggaaagccctggggcagcagcagcgaatgagtcacataatgggtccatctctc	577	
QY	541	cccatctctggagatggggagaagtgatatgaccttcatctgctgtgccagggaacct	600	
Db	578	cccatctctggagatggggagaagtgatatgaccttcatctgctgtgccagggaacct	637	
QY	601	gtcagcagaaaattctcaagcccatctctgtccagggaagctctgtgaaggtgctgtgat	660	
Db	638	gtcagcagaaaattctcaagcccatctctgtccagggaagctctgtgaaggtgctgtgat	697	
QY	661	gacccagattcctccatgggtcctctgtctctgttctgttggccctctctgctcagctctc	720	
Db	698	gacccagattcctccatgggtcctctgtctctgttctgttggccctctctgctcagctctc	757	
QY	721	tttgtactggggctattttttgtttctgaagagagagacagaagaagtacattgaa	780	
Db	758	tttgtactggggctattttttgtttctgaagagagagacagaagaagtacattgaa	817	
QY	781	gagaagaagagatgggacattgtcgggaaactcctaacatagcccccattctggagag	840	
Db	818	gagaagaagagatgggacattgtcgggaaactcctaacatagcccccattctggagag	877	
QY	841	aacacagagtagcacacaatccctccactaatagaacaatccttaaggagaatccagca	900	
Db	878	aacacagagtagcacacaatccctccactaatagaacaatccttaaggagaatccagca	937	
QY	901	aatacoggttactccactgtggaaataccgaaaaagatggaaaaatcccccaactgctc	960	
QY	938	aatacoggttactccactgtggaaataccgaaaaagatggaaaaatcccccaactgctc	997	
		cgatgcagacacacacaaagcctatttgcctatgagaatgttatctag	1008	
		gcagacacacaaagcctatttgcctatgagaatgttatctag	1045	